

## SEQUENCE LISTING

<110> Certa, U.  
Fingerle, J.  
Nelboeck-Hochste, P.  
Schoenfeld, H.

<120> MODIFIED PHOSPHODIESTERASE POLYPEPTIDES WITH ALTERED PHYSIOCHEMICAL  
PROPERTIES

<130> 21507

<150> 02028057.4

<151> 2002-12-17

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 673

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D3

<222> (1)..(673)

<220>

<221> LF1\_splice\_site

<222> (17)..(17)

<220>

<221> UCR1\_site\_-13

<222> (37)..(37)

<220>

<221> UCR1\_start

<222> (50)..(50)

<220>

<221> Ser54

<222> (54)..(54)

<220>

<221> Ser579

<222> (579)..(579)

<400> 1

Met Met His Val Asn Asn Phe Pro Phe Arg Arg His Ser Trp Ile Cys

1            5            10            15

Phe Asp Val Asp Asn Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro

20            25            30

Met Thr Ser Pro Gly Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His

35            40            45

Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp  
50 55 60

Leu Ser Pro Lys Ser Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile  
65 70 75 80

His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser  
85 90 95

Leu Arg Thr Val Arg Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp  
100 105 110

Arg Ala Pro Ser Lys Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn  
115 120 125

Lys Ala Thr Ile Thr Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr  
130 135 140

Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr  
145 150 155 160

Arg His Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu  
165 170 175

Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln  
180 185 190

Val Ser Glu Phe Ile Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val  
195 200 205

Glu Ile Pro Ser Pro Thr Gln Lys Glu Lys Glu Lys Lys Arg Pro  
210 215 220

Met Ser Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser Leu  
225 230 235 240

Thr Asn Ser Ser Ile Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp  
245 250 255

Val Leu Ala Lys Glu Leu Glu Asp Val Asn Lys Trp Gly Leu His Val  
260 265 270

Phe Arg Ile Ala Glu Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met  
275 280 285

His Thr Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro  
290 295 300

Val Asp Thr Leu Ile Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His  
305            310            315            320

Ala Asp Val Ala Tyr His Asn Asn Ile His Ala Ala Asp Val Val Gln  
             325            330            335

Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr  
             340            345            350

Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val  
             355            360            365

Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu  
             370            375            380

Leu Ala Leu Met Tyr Asn Asp Ser Ser Val Leu Glu Asn His His Leu  
385            390            395            400

Ala Val Gly Phe Lys Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln  
             405            410            415

Asn Leu Thr Lys Lys Gln Arg Gln Ser Leu Arg Lys Met Val Ile Asp

420 425 430

Ile Val Leu Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala Asp

435 440 445

Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu

450 455 460

Leu Leu Asp Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val

465 470 475 480

His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg

485 490 495

Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg

500 505 510

Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His Asn

515 520 525

Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His

530 535 540

Pro Leu Trp Glu Thr Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp  
545                550                555                560

Ile Leu Asp Thr Leu Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile  
                  565                570                575

Pro Gln Ser Pro Ser Pro Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln  
                  580                585                590

Gly Gln Thr Glu Lys Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly  
                  595                600                605

Glu Ser Asp Thr Glu Lys Asp Ser Gly Ser Gln Val Glu Glu Asp Thr  
                  610                615                620

Ser Cys Ser Asp Ser Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr  
625                630                635                640

Glu Ile Pro Leu Asp Glu Gln Val Glu Glu Glu Ala Val Gly Glu Glu  
                  645                650                655

Glu Glu Ser Gln Pro Glu Ala Cys Val Ile Asp Asp Arg Ser Pro Asp  
                  660                665                670

Thr

<210> 2

<211> 664

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D\_core

<222> (1)..(664)

<220>

<221> LF1\_splice\_site

<222> (2)..(2)

<220>

<221> UCR1\_site\_-13

<222> (22)..(22)

<220>

<221> UCR1\_site

<222> (35)..(35)

<220>

<221> SER54

<222> (39)..(39)



<220>

<221> SER579

<222> (564)..(564)

<400> 2

Met Phe Asp Val Asp Asn Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp

1            5            10            15

Pro Met Thr Ser Pro Gly Ser Gly Leu Ile Leu Gln Ala Asn Phe Val

20            25            30

His Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr

35            40            45

Asp Leu Ser Pro Lys Ser Met Ser Arg Asn Ser Ser Ile Ala Ser Asp

50            55            60

Ile His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala

65            70            75            80

Ser Leu Arg Thr Val Arg Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln

85            90            95

Asp Arg Ala Pro Ser Lys Arg Ser Pro Met Cys Asn Gln Pro Ser Ile

100 105 110

Asn Lys Ala Thr Ile Thr Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu

115 120 125

Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln

130 135 140

Thr Arg His Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met

145 150 155 160

Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn

165 170 175

Gln Val Ser Glu Phe Ile Ser Asn Thr Phe Leu Asp Lys Gln His Glu

180 185 190

Val Glu Ile Pro Ser Pro Thr Gln Lys Glu Lys Glu Lys Lys Arg

195 200 205

Pro Met Ser Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser

210 215 220

Leu Thr Asn Ser Ser Ile Pro Arg Phe Gly Val Lys Thr Glu Gln Glu  
225                230                235                240

Asp Val Leu Ala Lys Glu Leu Glu Asp Val Asn Lys Trp Gly Leu His  
                  245                250                255

Val Phe Arg Ile Ala Glu Leu Ser Gly Asn Arg Pro Leu Thr Val Ile  
                  260                265                270

Met His Thr Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile  
                  275                280                285

Pro Val Asp Thr Leu Ile Thr Tyr Leu Met Thr Leu Glu Asp His Tyr  
                  290                295                300

His Ala Asp Val Ala Tyr His Asn Asn Ile His Ala Ala Asp Val Val  
305                310                315                320

Gln Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Glu Ala Val Phe  
                  325                330                335

Thr Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ser Ala Ile His Asp  
                  340                345                350

Val Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser  
355 360 365

Glu Leu Ala Leu Met Tyr Asn Asp Ser Ser Val Leu Glu Asn His His  
370 375 380

Leu Ala Val Gly Phe Lys Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe  
385 390 395 400

Gln Asn Leu Thr Lys Lys Gln Arg Gln Ser Leu Arg Lys Met Val Ile  
405 410 415

Asp Ile Val Leu Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala  
420 425 430

Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val  
435 440 445

Leu Leu Leu Asp Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Met  
450 455 460

Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr  
465            470            475            480

Arg Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Arg Gln Gly Asp  
          485            490            495

Arg Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His  
          500            505            510

Asn Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val  
          515            520            525

His Pro Leu Trp Glu Thr Trp Ala Asp Leu Val His Pro Asp Ala Gln  
          530            535            540

Asp Ile Leu Asp Thr Leu Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr  
545            550            555            560

Ile Pro Gln Ser Pro Ser Pro Ala Pro Asp Asp Pro Glu Glu Gly Arg  
          565            570            575

Gln Gly Gln Thr Glu Lys Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp  
          580            585            590

Gly Glu Ser Asp Thr Glu Lys Asp Ser Gly Ser Gln Val Glu Glu Asp  
595 600 605

Thr Ser Cys Ser Asp Ser Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser  
610 615 620

Thr Glu Ile Pro Leu Asp Glu Gln Val Glu Glu Glu Ala Val Gly Glu  
625 630 635 640

Glu Glu Glu Ser Gln Pro Glu Ala Cys Val Ile Asp Asp Arg Ser Pro  
645 650 655

Asp Thr His His His His His His  
660

<210> 3

<211> 747

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D5

<222> (1)..(747)

<220>

<221> isoform\_specific\_N-terminus

<222> (1)..(90)

<220>

<221> LF1\_splice\_site

<222> (91)..(91)

<220>

<221> UCR1\_site-13

<222> (111)..(111)

<220>

<221> UCR1\_site

<222> (124)..(124)

<220>

<221> Ser54

<222> (128)..(128)

<220>

<221> Ser579

<222> (653)..(653)

<400> 3

Met Ala Gln Gln Thr Ser Pro Asp Thr Leu Thr Val Pro Glu Val Asp

1

5

10

15

Asn Pro His Cys Pro Asn Pro Trp Leu Asn Glu Asp Leu Val Lys Ser

20 25 30

Leu Arg Glu Asn Leu Leu Gln His Glu Lys Ser Lys Thr Ala Arg Lys

35 40 45

Ser Val Ser Pro Lys Leu Ser Pro Val Ile Ser Pro Arg Asn Ser Pro

50 55 60

Arg Leu Leu Arg Arg Met Leu Leu Ser Ser Asn Ile Pro Lys Gln Arg

65 70 75 80

Arg Phe Thr Val Ala His Thr Cys Lys Leu Phe Asp Val Asp Asn Gly

85 90 95

Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly Ser

100 105 110

Gly Leu Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu Ser

115 120 125

Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser Met

130 135 140



Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu Ile  
145            150            155            160

Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg Asn  
          165            170            175

Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys Arg  
          180            185            190

Ser Pro Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr Glu  
          195            200            205

Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp Trp  
          210            215            220

Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser Glu  
225            230            235            240

Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr His  
          245            250            255

Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile Ser  
260 265 270

Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro Thr  
275 280 285

Gln Lys Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser Gly  
290 295 300

Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile Pro  
305 310 315 320

Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu Leu  
325 330 335

Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu Leu  
340 345 350

Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln Glu  
355 360 365

Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile Thr  
370 375 380

Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr His  
385                    390                    395                    400

Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu Leu  
                  405                    410                    415

Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu Ala  
                  420                    425                    430

Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val Ser  
                  435                    440                    445

Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn  
                  450                    455                    460

Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys Leu  
465                    470                    475                    480

Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys Gln  
                  485                    490                    495

Arg Gln Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr Asp  
500 505 510

Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val Glu  
515 520 525

Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr Ser  
530 535 540

Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu Ser  
545 550 555 560

Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg Ile  
565 570 575

Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly Met  
580 585 590

Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys Ser  
595 600 605

Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp  
610 615 620

Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu  
625 630 635 640

Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser Pro  
645 650 655

Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys Phe  
660 665 670

Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu Lys  
675 680 685

Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser Lys  
690 695 700

Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp Glu  
705 710 715 720

Gln Val Glu Glu Glu Ala Val Gly Glu Glu Glu Glu Ser Gln Pro Glu  
725 730 735

Ala Cys Val Ile Asp Asp Arg Ser Pro Asp Thr  
740 745

<210> 4

<211> 689

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D6

<222> (1)..(689)

<220>

<221> isoform\_specific\_N-terminus

<222> (1)..(32)

<220>

<221> LF1\_splice\_site

<222> (33)..(33)

<220>

<221> UCR1\_start-13

<222> (53)..(53)

<220>

<221> UCR1\_start

<222> (66)..(66)

<220>

<221> Ser54

<222> (70)..(70)

<220>

<221> Ser579

<222> (595)..(595)

<400> 4

Met Ala Phe Val Trp Asp Pro Leu Gly Ala Thr Val Pro Gly Pro Ser

1            5            10            15

Thr Arg Ala Lys Ser Arg Leu Arg Phe Ser Lys Ser Tyr Ser Lys Leu

20            25            30

Phe Asp Val Asp Asn Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro

35            40            45

Met Thr Ser Pro Gly Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His

50            55            60

Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp

65            70            75            80

Leu Ser Pro Lys Ser Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile

85

90

95

His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser

100

105

110

Leu Arg Thr Val Arg Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp

115

120

125

Arg Ala Pro Ser Lys Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn

130

135

140

Lys Ala Thr Ile Thr Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr

145

150

155

160

Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr

165

170

175

Arg His Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu

180

185

190

Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln

195

200

205



Val Ser Glu Phe Ile Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val  
210 215 220

Glu Ile Pro Ser Pro Thr Gln Lys Glu Lys Glu Lys Lys Arg Pro  
225 230 235 240

Met Ser Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser Leu  
245 250 255

Thr Asn Ser Ser Ile Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp  
260 265 270

Val Leu Ala Lys Glu Leu Glu Asp Val Asn Lys Trp Gly Leu His Val  
275 280 285

Phe Arg Ile Ala Glu Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met  
290 295 300

His Thr Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro  
305 310 315 320

Val Asp Thr Leu Ile Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His  
325 330 335

Ala Asp Val Ala Tyr His Asn Asn Ile His Ala Ala Asp Val Val Gln  
340 345 350

Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr  
355 360 365

Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val  
370 375 380

Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu  
385 390 395 400

Leu Ala Leu Met Tyr Asn Asp Ser Ser Val Leu Glu Asn His His Leu  
405 410 415

Ala Val Gly Phe Lys Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln  
420 425 430

Asn Leu Thr Lys Lys Gln Arg Gln Ser Leu Arg Lys Met Val Ile Asp  
435 440 445

Ile Val Leu Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala Asp  
450 455 460

Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu  
465 470 475 480

Leu Leu Asp Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val  
485 490 495

His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg  
500 505 510

Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg  
515 520 525

Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His Asn  
530 535 540

Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His  
545 550 555 560

Pro Leu Trp Glu Thr Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp  
565 570 575

Ile Leu Asp Thr Leu Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile  
580 585 590

Pro Gln Ser Pro Ser Pro Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln  
595 600 605

Gly Gln Thr Glu Lys Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly  
610 615 620

Glu Ser Asp Thr Glu Lys Asp Ser Gly Ser Gln Val Glu Glu Asp Thr  
625 630 635 640

Ser Cys Ser Asp Ser Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr  
645 650 655

Glu Ile Pro Leu Asp Glu Gln Val Glu Glu Glu Ala Val Gly Glu Glu  
660 665 670

Glu Glu Ser Gln Pro Glu Ala Cys Val Ile Asp Asp Arg Ser Pro Asp  
675 680 685

Thr

<210> 5

<211> 750

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D7

<222> (1)..(750)

<220>

<221> isoform\_specific\_N-terminus

<222> (1)..(93)

<220>

<221> LF1\_splice\_site

<222> (94)..(94)

<220>

<221> UCR1\_start-13

<222> (114)..(114)

<220>

<221> UCR1\_start

<222> (127)..(127)

<220>

<221> Ser54

<222> (131)..(131)

<220>

<221> Ser579

<222> (656)..(656)

<400> 5

Met Lys Arg Asn Thr Cys Asp Leu Leu Ser Arg Ser Lys Ser Ala Ser  
1            5            10            15

Glu Glu Thr Leu His Ser Ser Asn Glu Glu Glu Asp Pro Phe Arg Gly  
          20            25            30

Met Glu Pro Tyr Leu Val Arg Arg Leu Ser Cys Arg Asn Ile Gln Leu  
          35            40            45

Pro Pro Leu Ala Phe Arg Gln Leu Glu Gln Ala Asp Leu Lys Ser Glu  
          50            55            60

Ser Glu Asn Ile Gln Arg Pro Thr Ser Leu Pro Leu Lys Ile Leu Pro  
65            70            75            80

Leu Ile Ala Ile Thr Ser Ala Glu Ser Ser Gly Lys Leu Phe Asp Val  
          85            90            95

Asp Asn Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser  
100 105 110

Pro Gly Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg  
115 120 125

Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro  
130 135 140

Lys Ser Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp  
145 150 155 160

Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr  
165 170 175

Val Arg Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro  
180 185 190

Ser Lys Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr  
195 200 205

Ile Thr Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu  
210 215 220

Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser  
225                    230                    235                    240

Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu  
                  245                    250                    255

Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu  
                  260                    265                    270

Phe Ile Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro  
                  275                    280                    285

Ser Pro Thr Gln Lys Glu Lys Glu Lys Lys Arg Pro Met Ser Gln  
                  290                    295                    300

Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser  
305                    310                    315                    320

Ser Ile Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala  
                  325                    330                    335

Lys Glu Leu Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile  
                  340                    345                    350



Ala Glu Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile  
355 360 365

Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr  
370 375 380

Leu Ile Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val  
385 390 395 400

Ala Tyr His Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His  
405 410 415

Val Leu Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu  
420 425 430

Ile Leu Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro  
435 440 445

Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu  
450 455 460

Met Tyr Asn Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly  
465                470                475                480

Phe Lys Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr  
                  485                490                495

Lys Lys Gln Arg Gln Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu  
                  500                505                510

Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr  
                  515                520                525

Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp  
                  530                535                540

Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala  
545                550                555                560

Asp Leu Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr  
                  565                570                575

Asp Arg Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu  
                  580                585                590

Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val  
595 600 605

Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp  
610 615 620

Glu Thr Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp  
625 630 635 640

Thr Leu Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser  
645 650 655

Pro Ser Pro Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr  
660 665 670

Glu Lys Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp  
675 680 685

Thr Glu Lys Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser  
690 695 700

Asp Ser Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro  
705            710            715            720

Leu Asp Glu Gln Val Glu Glu Glu Ala Val Gly Glu Glu Glu Ser  
725            730            735

Gln Pro Glu Ala Cys Val Ile Asp Asp Arg Ser Pro Asp Thr  
740            745            750

<210> 6

<211> 679

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D8

<222> (1)..(679)

<220>

<221> isoform\_specific\_N-terminus

<222> (1)..(23)

<220>

<221> LF1\_splice\_site

<222> (23)..(23)

<220>

<221> UCR1\_start-13

<222> (43)..(43)

<220>

<221> UCR1\_start

<222> (56)..(56)

<220>

<221> Ser54

<222> (60)..(60)

<220>

<221> Ser579

<222> (585)..(585)

<400> 6

Met Ser Ile Ile Met Lys Pro Arg Ser Arg Ser Thr Ser Ser Leu Arg

1            5            10            15

Thr Ala Glu Ala Lys Leu Phe Asp Val Asp Asn Gly Thr Ser Ala Gly

20            25            30

Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly Ser Gly Leu Ile Leu

35            40            45

Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg

50                      55                      60

Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser Met Ser Arg Asn Ser

65                      70                      75                      80

Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu Ile Val Thr Pro Phe

85                      90                      95

Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg Asn Asn Phe Ala Ala

100                      105                      110

Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys Arg Ser Pro Met Cys

115                      120                      125

Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr Glu Glu Ala Tyr Gln

130                      135                      140

Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln

145                      150                      155                      160

Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser Glu Met Ala Ser Asn

165                      170                      175

Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met  
180 185 190

Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile Ser Asn Thr Phe Leu  
195 200 205

Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro Thr Gln Lys Glu Lys  
210 215 220

Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser Gly Val Lys Lys Leu  
225 230 235 240

Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile Pro Arg Phe Gly Val  
245 250 255

Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu Leu Glu Asp Val Asn  
260 265 270

Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu Leu Ser Gly Asn Arg  
275 280 285

Pro Leu Thr Val Ile Met His Thr Ile Phe Gln Glu Arg Asp Leu Leu  
290 295 300

Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile Thr Tyr Leu Met Thr  
305            310            315            320

Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr His Asn Asn Ile His  
             325            330            335

Ala Ala Asp Val Val Gln Ser Thr His Val Leu Leu Ser Thr Pro Ala  
             340            345            350

Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala  
             355            360            365

Ser Ala Ile His Asp Val Asp His Pro Gly Val Ser Asn Gln Phe Leu  
             370            375            380

Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn Asp Ser Ser Val  
385            390            395            400

Leu Glu Asn His His Leu Ala Val Gly Phe Lys Leu Leu Gln Glu Glu  
             405            410            415



Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys Gln Arg Gln Ser Leu

420

425

430

Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr Asp Met Ser Lys His

435

440

445

Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val

450

455

460

Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr Ser Asp Arg Ile Gln

465

470

475

480

Val Leu Gln Asn Met Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys

485

490

495

Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg Ile Met Glu Glu Phe

500

505

510

Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly Met Glu Ile Ser Pro

515

520

525

Met Cys Asp Lys His Asn Ala Ser Val Glu Lys Ser Gln Val Gly Phe

530

535

540

Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp Ala Asp Leu Val  
545            550            555            560

His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu Asp Asn Arg Glu  
565            570            575

Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser Pro Ala Pro Asp Asp  
580            585            590

Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys Phe Gln Phe Glu Leu  
595            600            605

Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu Lys Asp Ser Gly Ser  
610            615            620

Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser Lys Thr Leu Cys Thr  
625            630            635            640

Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp Glu Gln Val Glu Glu  
645            650            655

Glu Ala Val Gly Glu Glu Glu Glu Ser Gln Pro Glu Ala Cys Val Ile  
660            665            670

Asp Asp Arg Ser Pro Asp Thr

675

<210> 7

<211> 809

<212> PRT

<213> Homo sapiens

<220>

<221> PDE4D4

<222> (1)..(809)

<220>

<221> LF1\_splice\_site

<222> (153)..(153)

<220>

<221> UCR1\_start\_-13

<222> (173)..(173)

<220>

<221> UCR\_1\_start

<222> (186)..(186)

<220>

<221> Ser54

<222> (190)..(190)

<220>

<221> Ser579

<222> (715)..(715)

<400> 7

Met Glu Ala Glu Gly Ser Ser Ala Pro Ala Arg Ala Gly Ser Gly Glu

1            5            10            15

Gly Ser Asp Ser Ala Gly Gly Ala Thr Leu Lys Ala Pro Lys His Leu

20            25            30

Trp Arg His Glu Gln His His Gln Tyr Pro Leu Arg Gln Pro Gln Phe

35            40            45

Arg Leu Leu His Pro His His His Leu Pro Pro Pro Pro Pro Pro Ser

50            55            60

Pro Gln Pro Gln Pro Gln Cys Pro Leu Gln Pro Pro Pro Pro Pro Pro

65            70            75            80

Leu Pro Pro Pro Pro Pro Pro Gly Ala Ala Arg Gly Arg Tyr Ala

85            90            95

Ser Ser Gly Ala Thr Gly Arg Val Arg His Arg Gly Tyr Ser Asp Thr  
100 105 110

Glu Arg Tyr Leu Tyr Cys Arg Ala Met Asp Arg Thr Ser Tyr Ala Val  
115 120 125

Glu Thr Gly His Arg Pro Gly Leu Lys Lys Ser Arg Met Ser Trp Pro  
130 135 140

Ser Ser Phe Gln Gly Leu Arg Arg Phe Asp Val Asp Asn Gly Thr Ser  
145 150 155 160

Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly Ser Gly Leu  
165 170 175

Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu Ser Phe Leu  
180 185 190

Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser Met Ser Arg  
195 200 205

Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu Ile Val Thr  
210 215 220

Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg Asn Asn Phe  
225            230            235            240

Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys Arg Ser Pro  
          245            250            255

Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr Glu Glu Ala  
          260            265            270

Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu  
          275            280            285

Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser Glu Met Ala  
          290            295            300

Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr His Leu Ser  
305            310            315            320

Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile Ser Asn Thr  
          325            330            335

Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro Thr Gln Lys  
          340            345            350

Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser Gly Val Lys  
355 360 365

Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile Pro Arg Phe  
370 375 380

Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu Leu Glu Asp  
385 390 395 400

Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu Leu Ser Gly  
405 410 415

Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln Glu Arg Asp  
420 425 430

Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile Thr Tyr Leu  
435 440 445

Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr His Asn Asn  
450 455 460

Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu Leu Ser Thr  
465            470            475            480

Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu Ala Ala Ile  
              485            490            495

Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val Ser Asn Gln  
              500            505            510

Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn Asp Ser  
              515            520            525

Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys Leu Leu Gln  
              530            535            540

Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys Gln Arg Gln  
545            550            555            560

Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr Asp Met Ser  
              565            570            575

Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val Glu Thr Lys  
              580            585            590



Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr Ser Asp Arg  
595 600 605

Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu Ser Asn Pro  
610 615 620

Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg Ile Met Glu  
625 630 635 640

Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly Met Glu Ile  
645 650 655

Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys Ser Gln Val  
660 665 670

Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp Ala Asp  
675 680 685

Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu Asp Asn  
690 695 700

Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser Pro Ala Pro  
705            710            715            720

Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys Phe Gln Phe  
725            730            735

Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu Lys Asp Ser  
740            745            750

Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser Lys Thr Leu  
755            760            765

Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp Glu Gln Val  
770            775            780

Glu Glu Glu Ala Val Gly Glu Glu Glu Glu Ser Gln Pro Glu Ala Cys  
785            790            795            800

Val Ile Asp Asp Arg Ser Pro Asp Thr  
805

<210> 8

<211> 1974

<212> DNA

<213> Homo sapiens

<220>

<221> PDE4D3\_coding\_sequence

<222> (1)..(1974)

<400> 8

tttgatgtgg acaatggcac atctgcggga cggagtcctt tggatcccat gaccagccca 60

ggatccgggc taattctcca agcaaatttt gtccacagtc aacgacggga gtccttctg 120

tatcgatccg acagcgatta tgacctctct ccaaagtcta tgtcccgga ctcctccatt 180

gccagtgata tacacggaga tgacttgatt gtgactccat ttgctcaggt cttggccagt 240

ctgcgaactg tacgaaacaa ctttgctgca ttaactaatt tgcaagatcg agcacctagc 300

aaaagatcac ccatgtgcaa ccaaccatcc atcaacaaag ccaccataac agaggaggcc 360

taccagaaac tggccagcga gacctggag gagctggact ggtgtctgga ccagctagag 420

accctacaga ccaggcactc cgtcagtgag atggcctcca acaagtttaa aaggatgctt 480

aatcgggagc tcacccatct ctctgaaatg agtcggtctg gaaatcaagt gtcagagttt 540

atatcaaaca cattcttaga taagcaacat gaagtggaaa ttcttctcc aactcagaag 600

gaaaaggaga aaaagaaaag accaatgtct cagatcagtg gagtcaagaa attgatgcac 660

agctctagtc tgactaattc aagtatccca aggtttggag ttaaaactga acaagaagat 720  
 gtcttgcca aggaactaga agatgtgaac aaatggggtc ttcatgtttt cagaatagca 780  
 gagttgtctg gtaaccggcc ctgactgtt atcatgcaca ccattttca ggaacgggat 840  
 ttattaaaa catttaaat tccagtagat actttaatta catatcttat gactctgaa 900  
 gaccattacc atgctgatgt ggcctatcac aacaatatcc atgctgcaga tgtgtccag 960  
 tctactcatg tgctattatc tacacctgct ttggaggctg tgtttacaga tttggagatt 1020  
 ctgcagcaa ttttgccag tgcaatacat gatgtagatc atcctgggtg gtccaatcaa 1080  
 tttctgatca atacaaactc tgaactgcc ttgatgtaca atgattctc agtcttagag 1140  
 aaccatcatt tggctgtggg ctftaaattg cttcaggaag aaaactgtga cattttccag 1200  
 aattgacca aaaaacaaag acaatcttta aggaaaatgg tcattgacat cgtacttgca 1260  
 acagatatgt caaaacacat gaatctactg gctgatttga agactatggt tgaaactaag 1320  
 aaagtgacaa gctctggagt tcttcttctt gataattatt ccgataggat tcaggttctt 1380  
 cagaatatgg tgactgtgc agatctgagc aaccaacaa agcctctcca gctgtaccgc 1440  
 cagtgacgg accggataat ggaggagttc ttccgccaag gagaccgaga gagggaacgt 1500  
 ggcatggaga taagcccat gtgtgacaag cacaatgctt ccgtggaaaa atcacaggtg 1560  
 ggcttcatag actatattgt tcatcccctc tgggagacat gggcagacct cgtccaccct 1620

gacgcccagg atattttgga cactttggag gacaatcgtg aatggtacca gagcacaatc 1680

cctcagagcc cctctcctgc acctgatgac ccagaggagg gccggcaggg tcaaactgag 1740

aaattccagt ttgaactaac ttagaggaa gatggtgagt cagacacgga aaaggacagt 1800

ggcagtcaag tggaagaaga cactagctgc agtgactcca agactctttg tactcaagac 1860

tcagagtcta ctgaaattcc cttgatgaa caggttgaag aggaggcagt aggggaagaa 1920

gaggaaagcc agcctgaagc ctgtgtcata gatgatcgtt ctctgacac gtaa 1974

<210> 9

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> 5' primer

<222> (1)..(36)

<400> 9

gatgaattca agctttttga tgtggacaat ggcaca

36

<210> 10

<211> 45

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> 3' primer

<222> (1)..(45)

<400> 10

gtgatatctc attatcacgt gtcaggagaa cgatcatcta tgaca 45

<210> 11

<211> 61

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> 6His

<222> (1)..(61)

<400> 11

gtgatatctc attatcaatg ggatggatgat ggtgcgtgtc aggagaacga tcatctatga 60

c

61